RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/528,844,
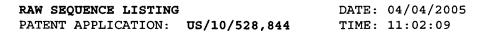Source: PCT/10
Date Processed by STIC: 4/4/05

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PCT

RAW SEQUENCE LISTING   DATE: 04/04/2005
PATENT APPLICATION: US/10/528,844   TIME: 11:02:09

Input Set : **A:\0185658SeqList.txt**
Output Set: **N:\CRF4\04042005\J528844.raw**

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   3 <110> APPLICANT: F. HOFFMANN-LA ROCHE AG
   5 <120> TITLE OF INVENTION: DNA encoding FAD dependent D-erythronic acid
   6       4-phospohate dehydrogenase involved in vitamin B6
   7       biosynthesis
   9 <130> FILE REFERENCE: sequence for pdxR (case19)
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/528,844
C--> 12 <141> CURRENT FILING DATE: 2005-03-23
  14 <160> NUMBER OF SEQ ID NOS: 4
  16 <170> SOFTWARE: PatentIn Ver. 2.1
  18 <210> SEQ ID NO: 1
  19 <211> LENGTH: 1491
  20 <212> TYPE: DNA
  21 <213> ORGANISM: Sinorhizobium meliloti
  23 <400> SEQUENCE: 1
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  26 accgcacccg ccgacacggc accctacctc gtcgagtccc gcgggctcta ccgcggcacg   180
  27 acgccgctcg tgctcaggcc cggctccgtc gaggaagttt cgctggtgat gcggcttgcg   240
  28 agtcagaccc gaacggcagt cgtgccgcag ggcggcaata ccggacatgt ggccggacag   300
  29 attccacgcg agggcaaagc cgacgtggtc cttccctcg agcggctgaa ccgcatccgc    360
  30 gacatcgacc cggtcggcaa cgtgatcgtg gccgacgccg ctgtatcct ggcggacatc    420
  31 cagaaggccg ccgatgacgt cgaccggctt tttcccctgt cactcggctc ggaaggctct   480
  32 gcccggatcg gcggcaatct ttcgaccaat gccggcggca ctgccgtgct tgcctatggg   540
  33 aacatgcgcc agctctgcct ggggctggaa gtcgtgctcc cgaccgggga gatctgggat   600
  34 gggctcagac gcctcaggaa ggacaatacc ggctacgatc tgcgcgatct tttcatcggc   660
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  36 ggccaccagg tggcctttgc cggcctcagg agcgtcgagg acgcacttac gcttttcgat   780
  37 cgggcaacaa gcgtctgcgg gccggccctg acgggcttcg aactgatgcc gcggctcggc   840
  38 atcgagttca ccacccggca catcgccggc gtcagagatc cgatggaaac gacgcatccg    900
  39 tggtacgcgc tgatcgatat ctccacctcg gataccgccg aaagcgcgga acggatggtg   960
  40 caagaccttc tcgaagccgt cattgccgac ggtctcgtcg aaaacgcggt catcgcccag   1020
  41 aacgaagcgc aacgcagagc gctctggcac atgcgagaaa gcatgtcgcc ggcacaaaag  1080
  42 cctgagggtg gctccatcaa gcatgacgtt tcggtcccgg tgtcgagcat ccggccttc   1140
  43 atgacggagg cggatgcgct ggtctccaag gccatccccg gcgcgcgcat ctgcgccttc  1200
  44 ggccatatgg gcgacggcaa tatccactac aacatctccc agcccgtcgg cgcggacaag  1260
  45 cagagctttc tcgatcggtg gcgcgagatc aatgcgatcg ttcacgccgt cgtgctcaaa  1320
  46 catgacggct cgatctctgc cgagcatggc atcggccagt tgaagcgaga cgaactcgcg  1380
  47 gcgatccgct cgccgatcga gatcgagctc atgcgacgga tcaagcacgc cttcgacccg  1440
  48 gcggggatca tgaacccccga taaggtgctg cgcgaggatc gaggcgagta a            1491
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  52 <211> LENGTH: 496
  53 <212> TYPE: PRT
  54 <213> ORGANISM: Sinorhizobium meliloti
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60                  20                  25                  30
61 Ile Val Gly Pro Gly Asn Ala Leu Thr Ala Pro Ala Asp Thr Ala Pro
62              35                  40                  45
63 Tyr Leu Val Glu Ser Arg Gly Leu Tyr Arg Gly Thr Thr Pro Leu Val
64      50                  55                   60
65 Leu Arg Pro Gly Ser Val Glu Glu Val Ser Leu Val Met Arg Leu Ala
66 65                  70                  75                  80
67 Ser Gln Thr Arg Thr Ala Val Val Pro Gln Gly Gly Asn Thr Gly His
68                  85                  90                  95
69 Val Ala Gly Gln Ile Pro Arg Glu Gly Lys Ala Asp Val Val Leu Ser
70              100                 105                 110
71 Leu Glu Arg Leu Asn Arg Ile Arg Asp Ile Asp Pro Val Gly Asn Val
72              115                 120                 125
73 Ile Val Ala Asp Ala Gly Cys Ile Leu Ala Asp Ile Gln Lys Ala Ala
74      130                 135                 140
75 Asp Asp Val Asp Arg Leu Phe Pro Leu Ser Leu Gly Ser Glu Gly Ser
76 145                 150                 155                 160
77 Ala Arg Ile Gly Gly Asn Leu Ser Thr Asn Ala Gly Gly Thr Ala Val
78              165                 170                 175
79 Leu Ala Tyr Gly Asn Met Arg Gln Leu Cys Leu Gly Leu Glu Val Val
80              180                 185                 190
81 Leu Pro Thr Gly Glu Ile Trp Asp Gly Leu Arg Arg Leu Arg Lys Asp
82              195                 200                 205
83 Asn Thr Gly Tyr Asp Leu Arg Asp Leu Phe Ile Gly Ala Glu Gly Thr
84      210                 215                 220
85 Leu Gly Val Ile Thr Gly Ala Val Leu Lys Leu Phe Pro Lys Pro Arg
86 225                 230                 235                 240
87 Gly His Gln Val Ala Phe Ala Gly Leu Arg Ser Val Glu Asp Ala Leu
88              245                 250                 255
89 Thr Leu Phe Asp Arg Ala Thr Ser Val Cys Gly Pro Ala Leu Thr Gly
90              260                 265                 270
91 Phe Glu Leu Met Pro Arg Leu Gly Ile Glu Phe Thr Thr Arg His Ile
92              275                 280                 285
93 Ala Gly Val Arg Asp Pro Met Glu Thr Thr His Pro  Trp Tyr Ala Leu
94      290                 295                 300
95 Ile Asp Ile Ser Thr Ser Asp Thr Ala Glu Ser Ala Glu Arg Met Val
96 305                 310                 315                 320
97 Gln Asp Leu Leu Glu Ala Val Ile Ala Asp Gly Leu Val Glu Asn Ala
98              325                 330                 335
99 Val Ile Ala Gln Asn Glu Ala Gln Arg Arg Ala Leu Trp His Met Arg
100             340                 345                 350
101 Glu Ser Met Ser Pro Ala Gln Lys Pro Glu Gly Gly Ser Ile Lys His
102             355                 360                 365
103 Asp Val Ser Val Pro Val Ser Ser Ile Pro Ala Phe Met Thr Glu Ala
104             370                 375                 380
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105 Asp Ala Leu Val Ser Lys Ala Ile Pro Gly Ala Arg Ile Cys Ala Phe
106 385                 390             395                 400
107 Gly His Met Gly Asp Gly Asn Ile His Tyr Asn Ile Ser Gln Pro Val
108             405             410             415
109 Gly Ala Asp Lys Gln Ser Phe Leu Asp Arg Trp Arg Glu Ile Asn Ala
110             420             425             430
111 Ile Val His Ala Val Val Leu Lys His Asp Gly Ser Ile Ser Ala Glu
112         435             440             445
113 His Gly Ile Gly Gln Leu Lys Arg Asp Glu Leu Ala Ala Ile Arg Ser
114     450             455             460
115 Pro Ile Glu Ile Glu Leu Met Arg Arg Ile Lys His Ala Phe Asp Pro
116 465             470             475                 480
117 Ala Gly Ile Met Asn Pro Asp Lys Val Leu Arg Glu Asp Arg Gly Glu
118             485             490             495
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122 <211> LENGTH: 19
123 <212> TYPE: DNA
124 <213> ORGANISM: Artificial Sequence
126 <220> FEATURE:
127 <223> OTHER INFORMATION: Description of Artificial Sequence:an artificially
128       synthesized primer sequence
130 <400> SEQUENCE: 3
131 gaattcatgg ccatcggca                                          19
134 <210> SEQ ID NO: 4
135 <211> LENGTH: 23
136 <212> TYPE: DNA
137 <213> ORGANISM: Artificial Sequence
139 <220> FEATURE:
140 <223> OTHER INFORMATION: Description of Artificial Sequence:an artificially
141       synthesized primer sequence
143 <400> SEQUENCE: 4
144 ccacttccct tgtagtacga gct                                     23
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VERIFICATION SUMMARY   DATE: 04/04/2005
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L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date